

click here to
toggle between
menus and buttons

Version 3.2

Optimal Global Sequence Alignment

- 51-02 SEQ ID NO:10 human mature BMP-11 NT
- 51-02 SEQ ID NO:1 bovine mature BMP-11 NT

```
ALIGN calculates a global alignment of two sequences
  version 2.0uPlease cite: Myers and Miller, CABIOS (1989) 4:11-17
51-02_SEQ_ID_NO:10human_mature_BMP-11 NT          327 nt vs.
51-02_SEQ_ID_NO:11bovine_mature_BMP-11 NT          327 nt
scoring matrix: DNA, gap penalties: -16/-4
92.7% identity;          Global alignment score: 1419
```

1 of 2

```
51-02_SEQ_ID  ATGGTGGTGGATCGCTGTGGCTGCTCT
               ::::::::::::::::::::::::::::
51-02_SEQ_ID  ATGGTGGTGGATCGCTGTGGCTGCTCC
               310           320
```

Import Alignment(s)	Return	Help	Report Bugs
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Citation

Algorithm Citation:

E. W. Myers and W. Miller, (1989) CABIOS 4:11-17.

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448.

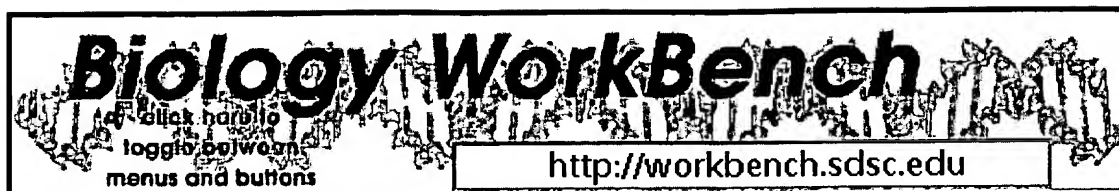
W. R. Pearson (1990) "Rapid and Sensitive Sequence Comparison with FASTP and FASTA" Methods in Enzymology 183:63-98).

Program Citation:

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SDSC



Version 3.2

ALIGN

Optimal Global Sequence Alignment

Selected Sequence(s)

- SEQ ID NO:1 nt 393-698
- SEQ ID NO:10 nt 778-1083

	Import Alignment(s)	Return	Help	Report Bugs	
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ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989) 4:11-17
 SEQ_ID_NO:1_nt_393-698 306 nt vs.
 SEQ_ID_NO:10_nt_778-1083 306 nt
 scoring matrix: DNA, gap penalties: -16/-4
 92.8% identity; Global alignment score: 1332

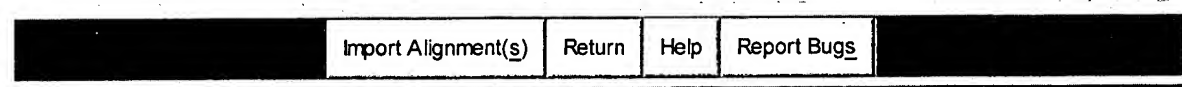
	10	20	30	40	50	60
SEQ_ID_NO:1_	GATGAACATTCAAGTGAGTCCCGCTGTTGCCGCTACCCCTCACTGTGGACTTTGAGGCT					
SEQ_ID_NO:10	GACGAGCACTCAAGCGAGTCCCGCTGCTGCCGATATCCCTCACAGTGGACTTTGAGGCT					
	10	20	30	40	50	60
SEQ_ID_NO:1_	TTTGGCTGGGACTGGATCATCGCTCCTAAACGCTACAAGGCCAACTACTGCTCCGGCCAG					
SEQ_ID_NO:10	TTCGGCTGGGACTGGATCATCGCACCTAAGCGCTACAAGGCCAACTACTGCTCCGGCCAG					
	70	80	90	100	110	120
SEQ_ID_NO:1_	TGCGAGTACATGTTTATGCAAAAGTATCCGCACACCCACTTGGTGCAACAGGCTAACCCA					
SEQ_ID_NO:10	TGCGAGTACATGTTTCATGCAAAAATATCCGCATACCCATTTGGTGCGAGCAGGCCAATCCA					
	130	140	150	160	170	180
SEQ_ID_NO:1_	AGAGGCTCTGCGGGGCCCTGCTGCACACCCACCAAGATGTCCCAATCAACATGCTCTAC					
SEQ_ID_NO:10	AGAGGCTCTGCTGGGGCCCTGTTGTACCCCAACCAAGATGTCCCAATCAACATGCTCTAC					
	190	200	210	220	230	240

```

                250      260      270      280      290      300
SEQ_ID_NO:1_   TTCAATGACAAGCAGCAGATTATCTACGGCAAGATCCCTGGCATGGTGGTGGATCGCTGT
                :
                :
                :
SEQ_ID_NO:10   TTCAATGACAAGCAGCAGATTATCTACGGCAAGATCCCTGGCATGGTGGTGGATCGCTGT
                250      260      270      280      290      300

SEQ_ID_NO:1_   GGCTGC
                :
                :
SEQ_ID_NO:10   GGCTGC

```



Citation

Algorithm Citation:

E. W. Myers and W. Miller, (1989) CABIOS 4:11-17.

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448.

W. R. Pearson (1990) "Rapid and Sensitive Sequence Comparison with FASTP and FASTA" Methods in Enzymology 183:63-98).

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